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Search	Most Recent Queries	Time	Result
#19	Search **35C1 antibody**	15:33:42	1
#17	Search **(breast-tumor-amplified kinase) and (monoclonal or Ig or antibody)**	15:31:56	45
#16	Search **(hark1) and (monoclonal or Ig or antibody)**	15:30:18	0
#15	Search **(aurora-related kinase 1) and (monoclonal or Ig or antibody)**	15:29:53	0
#14	Search **(aurora/ipl1-related kinase 1) and (monoclonal or Ig or antibody)**	15:28:48	4
#12	Search **(serine/threonine kinase 15) and (monoclonal or Ig or antibody)**	15:27:33	29
#10	Search **(serine/threonine kinase 15) or (aurora/ipl1-related kinase 1) or (aurora-related kinase 1) or (hark1) or (breast-tumor-amplified kinase) and monoclonal**	15:22:51	16
#9	Search **(serine/threonine kinase 15) or (aurora/ipl1-related kinase 1) or (aurora-related kinase 1) or (hark1) or (breast-tumor-amplified kinase)**	15:22:38	898
#8	Search **#7 and monoclonal**	15:19:40	5
#7	Search **aurora-A**	15:13:11	369
#6	Search **TACI-Ig and non-hodgkin's**	09:01:20	0
#5	Search **TACI-Fc and non-hodgkin's**	09:01:13	0
#3	Search **TACI-Fc and lymphoma**	08:59:04	2
#1	Search **TACI-Ig or TACI-Fc and non-hodgkin's**	08:56:32	10

Clear History

synonym search

Complex(kinase/cell division protein)

Biological unit = asymmetric unit, as shown (as defined in PDB file)

Jmol

Contents

- **Description**
  - **Header details**
  - Header records
  - References
  - PROCHECK
- **Protein chains**
  - A 266 a.a. *
  - B 30 a.a. *
- **Ligands**

PDB id: 1ol5
Name: Complex(kinase/cell division protein)
Title: Structure of **aurora-a** 122-403, phosphorylated on thr287, thr288 and bound to tpx2 1-43
Structure: Serine/threonine kinase 6. Synonym: **aurora-a**, serine/threonine kinase 15, aurora/ipl1-related kinase 1, aurora-related kinase 1, hark1, breast-tumor-amplified kinase. Chain: a. Fragment: catalytic domain residues 122 403. Engineered: yes. Other_details: phosphorylated on thr287, thr288. Restricted expression proliferation associated
Source: Homo sapiens. Human. Expressed in: escherichia coli.
Biological unit: Dimer (from PDB file)
UniProt: **Chain A:** Q14965 (STK6_HUMAN) [Pfam]

Seq:
Struc:
Seq: 403 a
Struc: 266 a

Chain B: Q9ULW0 (TPX2_HUMAN) [Pfam]

Seq:
Struc:
Seq:
Struc:
Seq: 747 a
Struc: 30 a.

* PDB and UniProt seqs differ at 2 residue positions (black crosses)

Metal ions
MG ×3

Waters ×144

* Residue conservation analysis

Tools
Image Generation
AstexViewer™@MSD-EBI
Run PROCHECK
Clefts Calculation

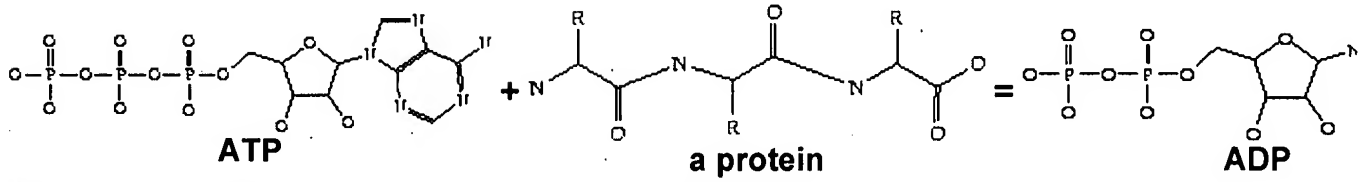
Enzyme class: Chain A: E.C.2.7.1.37 [IntEnz] [ExPASy] [KEGG] [BRENDA]
Reaction: ATP + a protein = ADP + a phosphoprotein (see diagram below)
Function: (see GO annotation below)
Resolution: 2.50Å
R-factor: 0.194
R-free: 0.252
Authors: R.Bayliss,E.Conti
Key ref: R.Bayliss et al. (2003). Structural basis of **Aurora-A** activation by TPX2 at the mitotic spindle.. *Mol Cell*, **12**, 851-862. [PubMed id: 14580337] [DOI: 10.1016/S1097-2765(00392-7]
Date: 06-Aug-03
Release date: 30-Oct-03
Related entries: 1muo crystal structure of aurora-2, an oncogenic serine-threonine kinase
1ol6 structure of unphosphorylated d274n mutant of **aurora**
1ol7 structure of human **aurora-a** 122-403 phosphorylated on thr287, thr288

Gene Ontology (GO) functional annotation

Biological process	protein amino acid phosphorylation	1 term(s)
Biochemical function	protein kinase activity	3 term(s)

For full annotation, click on icon

Enzyme reaction for E.C.2.7.1.37



Molecule diagrams generated from .mol files obtained from the KEGG ftp site.

Key ref
Mol Cell **12**:85

DOI no: 10.1016/S1097-2765(03)00392-7
PubMed id: 14580337

Structural basis of Aurora-A activation by TPX2 at the mitotic spindle

R.Bayliss, T.Sardon, I.Vernos, E.Conti.

ABSTRACT

Aurora-A is an oncogenic kinase essential for mitotic spindle assembly. It is activated by phosphorylation and by the microtubule-associated protein TPX2, which also localizes the kinase to spindle microtubules. We have uncovered the

olecular mechanism of Aurora-A activation by determining crystal structures of its phosphorylated form both with and residue long domain of TPX2 that we identified as fully functional for kinase activation and protection dephosphorylation. In the absence of TPX2, the Aurora-A activation segment is in an inactive conformation, with the cru phosphothreonine exposed and accessible for deactivation. Binding of TPX2 triggers no global conformational changes kinase but pulls on the activation segment, swinging the phosphothreonine into a buried position and locking the active conformation. The recognition between Aurora-A and TPX2 resembles that between the cAPK catalytic core and its flan regions, suggesting this molecular mechanism may be a recurring theme in kinase regulation.

Selected figure(s)

Figure 3.

Figure 3. Structure of Aurora-A Bound to TPX2(A) View of the complex between the catalytic domain of human Aurora (AuroraΔN, yellow) and the N-terminal domain of TPX2 shown in typical kinase orientation. An upstream stretch of TPX2 (red) binds at the N-terminal lobe of Aurora-A, and a downstream stretch (pink) binds between the two lobes. A dotted line in pink marks the approximate path of the linker connecting the two TPX2 stretches (disordered and not modeled).(B) View of the complex after a 180° rotation about the vertical axis in respect to view in (A) shows more clearly the two stretches of TPX2 binding to Aurora-A.(C) The upstream stretch of TPX2 (red, residues 7–21^TPX) binds at a hydrophobic surface groove present in the N-terminal lobe of the kinase (gray cartoon, yellow side chains). Details of the extensive interactions are shown in the same orientation as in (B). Aurora-A residues are labeled in black, and TPX2 residue labels are color coded as the structure.(D) The downstream helical stretch of TPX2 (pink, residues 30–43^TPX) binds Aurora-A near helix αC and the activation segment, close to but not directly in contact with phospho-Thr288^AUR (green). Details of interactions are shown in the same orientation as in (B) and (C).

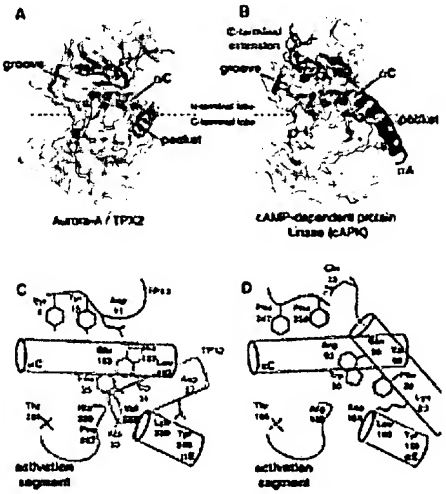


Figure 5.

Figure 5. TPX2-Aurora-A Intermolecular Interactions Resemble cAP Interactions(A and B) Transparent surfaces representing the conser cores of (A) Aurora-A and (B) cAPK show similar surface grooves ir lobe (between helix αC and the β sheet, gray cartoon) and a similar the two lobes (formed by the activation segment and helix αC, gray portions of TPX2 binding to Aurora-A are shown in red and pink (A), C-terminal extensions to the cAPK catalytic core are shown in light l D) Schematic diagram of the intermolecular interactions between Au TPX2 (pink and red) and of the cAPK intramolecular interactions (lig that their mode of recognition at the atomic level is rather similar. Th interactions of Tyr8^TPX, Tyr10^TPX, Trp34^TPX, and Phe35^TPX recapitulated by Phe347^cAPK, Phe350^cAPK, Trp30^cAPK, and F

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☐	L5	L3 and aurora-A kinase	0
☐	L4	L3 and aurora-A	1
☐	L3	L2 and (monoclonal or Ig or antibody)	38
☐	L2	(serine/threonine kinase 15) or (aurora/ipl1-related kinase 1) or (aurora-related kinase 1) or (hark1) or (breast-tumor-amplified kinase)	39
		DB=PGPB,USPT; PLUR=YES; OP=ADJ	
☐	L1	(serine/threonine kinase 15) or (aurora/ipl1-related kinase 1) or (aurora-related kinase 1) or (hark1) or (breast-tumor-amplified kinase)	39

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